

# RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/776,330A  
Source: 1Fw/6  
Date Processed by STIC: 9/15/06

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 09/15/2006

PATENT APPLICATION: US/10/776,330A

TIME: 11:56:29

Input Set : A:\50810531.APP

Output Set: N:\CRF4\09152006\J776330A.raw

```

3 <110> APPLICANT: GALZI, JEAN-LUC
4 ALIX, PHILIPPE
6 <120> TITLE OF INVENTION: USE OF A FLUORESCENT PROTEIN FOR DETECTING INTERACTION
7 BETWEEN A TARGET PROTEIN AND ITS LIGAND
9 <130> FILE REFERENCE: 0508-1053-1
11 <140> CURRENT APPLICATION NUMBER: 10/776,330A
12 <141> CURRENT FILING DATE: 2004-02-12
14 <150> PRIOR APPLICATION NUMBER: 09/445,205
15 <151> PRIOR FILING DATE: 2000-01-07
17 <150> PRIOR APPLICATION NUMBER: PCT/FR98/01136
18 <151> PRIOR FILING DATE: 1998-06-04
20 <150> PRIOR APPLICATION NUMBER: FR 97/06977
21 <151> PRIOR FILING DATE: 1997-06-05
23 <160> NUMBER OF SEQ ID NOS: 25
25 <170> SOFTWARE: PatentIn Ver. 3.2
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 798
29 <212> TYPE: DNA
30 <213> ORGANISM: Aequorea victoria
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(795)
36 <400> SEQUENCE: 1
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38 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
39 1 5 10 15
41 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
42 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
43 20 25 30
45 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
46 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
47 35 40 45
49 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
50 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
51 50 55 60
53 ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc aac cac atg aag      240
54 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
55 65 70 75 80
57 cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
58 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
59 85 90 95
61 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
62 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

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63          100          105          110
65 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
66 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
67          115          120          125
69 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
70 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
71          130          135          140
73 aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
74 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
75 145          150          155          160
77 ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
78 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
79          165          170          175
81 gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576
82 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
83          180          185          190
85 ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg 624
86 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
87          195          200          205
89 agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672
90 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
91          210          215          220
93 gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tac 720
94 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Tyr
95 225          230          235          240
97 tca gat ctc gag ctc aag ctt cga att ctg cag tcg acg gta ccg cgg 768
98 Ser Asp Leu Glu Leu Lys Leu Arg Ile Leu Gln Ser Thr Val Pro Arg
99          245          250          255
101 gcc cgg gat cca ccg gat cta gat aac tga 798
102 Ala Arg Asp Pro Pro Asp Leu Asp Asn
103          260          265
106 <210> SEQ ID NO: 2
107 <211> LENGTH: 265
108 <212> TYPE: PRT
109 <213> ORGANISM: Aequorea victoria
111 <400> SEQUENCE: 2
112 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
113 1          5          10          15
115 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
116          20          25          30
118 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
119          35          40          45
121 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
122          50          55          60
124 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
125 65          70          75          80
127 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
128          85          90          95
130 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

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131          100          105          110
133 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
134          115          120          125
136 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
137          130          135          140
139 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
140 145          150          155          160
142 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
143          165          170          175
145 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
146          180          185          190
148 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
149          195          200          205
151 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
152          210          215          220
154 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Tyr
155 225          230          235          240
157 Ser Asp Leu Glu Leu Lys Leu Arg Ile Leu Gln Ser Thr Val Pro Arg
158          245          250          255
160 Ala Arg Asp Pro Pro Asp Leu Asp Asn
161          260          265
164 <210> SEQ ID NO: 3
165 <211> LENGTH: 5
166 <212> TYPE: PRT
167 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
170 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic spacer
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173 Gly Gly Gly Gly Ser
174 1 5
179 <210> SEQ ID NO: 4
180 <211> LENGTH: 6
181 <212> TYPE: PRT
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic cyclopeptide
187 <400> SEQUENCE: 4
188 Gln Trp Phe Gly Leu Met
189 1 5
192 <210> SEQ ID NO: 5
193 <211> LENGTH: 29
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide
200 <400> SEQUENCE: 5
201 ggtcgccacc ctgtacaaga agggcgagg
204 <210> SEQ ID NO: 6
205 <211> LENGTH: 36

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206 <212> TYPE: DNA  
 207 <213> ORGANISM: Artificial Sequence  
 209 <220> FEATURE:  
 210 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
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 212 <400> SEQUENCE: 6  
 213 cacgagagga tgtagaacct cgaagcgacaca gtcacc 35  
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 217 <211> LENGTH: 44  
 218 <212> TYPE: DNA  
 219 <213> ORGANISM: Artificial Sequence  
 221 <220> FEATURE:  
 222 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
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 224 <400> SEQUENCE: 7  
 225 gtacccagac accagctagc agatctgaag cttcgccatc aggc 44  
 228 <210> SEQ ID NO: 8  
 229 <211> LENGTH: 39  
 230 <212> TYPE: DNA  
 231 <213> ORGANISM: Artificial Sequence  
 233 <220> FEATURE:  
 234 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
 236 <400> SEQUENCE: 8  
 237 ggagagttcc aactcgagaa aagaaagaag ggcgaggag 39  
 240 <210> SEQ ID NO: 9  
 241 <211> LENGTH: 36  
 242 <212> TYPE: DNA  
 243 <213> ORGANISM: Artificial Sequence  
 245 <220> FEATURE:  
 246 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
 248 <400> SEQUENCE: 9  
 249 gtcagctgtt tctgcggcgc gctaagcctg ggcctt 36  
 252 <210> SEQ ID NO: 10  
 253 <211> LENGTH: 51  
 254 <212> TYPE: DNA  
 255 <213> ORGANISM: Artificial Sequence  
 257 <220> FEATURE:  
 258 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
 260 <400> SEQUENCE: 10  
 261 ttagttctaa actagcggcc gcactagtcc tccatgaaca cttcagcccc a 51  
 264 <210> SEQ ID NO: 11  
 265 <211> LENGTH: 42  
 266 <212> TYPE: DNA  
 267 <213> ORGANISM: Artificial Sequence  
 269 <220> FEATURE:  
 270 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
 272 <400> SEQUENCE: 11  
 273 cttgaacctta tagctagcct cgagtcagca ttggcgggag gg 42  
 276 <210> SEQ ID NO: 12  
 277 <211> LENGTH: 28  
 278 <212> TYPE: DNA

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279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
282 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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284 <400> SEQUENCE: 12
285 cctgctgtct cagatctcat caccgtcc 28
288 <210> SEQ ID NO: 13
289 <211> LENGTH: 47
290 <212> TYPE: DNA
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide
296 <400> SEQUENCE: 13
297 cagatcatta gttgtacagg aaagatcttg aggatcctgg agtgaag 47
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301 <211> LENGTH: 29
302 <212> TYPE: DNA
303 <213> ORGANISM: Artificial Sequence
305 <220> FEATURE:
306 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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308 <400> SEQUENCE: 14
309 ggcccaagct tatgtcagga tccggggat 29
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313 <211> LENGTH: 30
314 <212> TYPE: DNA
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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320 <400> SEQUENCE: 15
321 cgcccgctcg agtcacaagc ccacagatat 30
324 <210> SEQ ID NO: 16
325 <211> LENGTH: 21
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329 <220> FEATURE:
330 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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336 <210> SEQ ID NO: 17
337 <211> LENGTH: 78
338 <212> TYPE: DNA
339 <213> ORGANISM: Artificial Sequence
341 <220> FEATURE:
342 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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345 <400> SEQUENCE: 17
346 agcacagagg gcagtagcaa tgaggatgac agcgaggcgt gccgcggaga ccttcattgg 60
347 atcccgaagc ttatcaac 78
350 <210> SEQ ID NO: 18

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351 <211> LENGTH: 78  
352 <212> TYPE: DNA

**VERIFICATION SUMMARY**

DATE: 09/15/2006

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